

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

[rtracklayer](#)

RRID:SCR_021325

Type: Tool

Proper Citation

rtracklayer (RRID:SCR_021325)

Resource Information

URL: <https://bioconductor.org/packages/rtracklayer/>

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Description: Software R package for interfacing with genome browsers. Supports integration of existing genome browsers with experimental data analyses performed in R. R interface to genome annotation files and UCSC genome browser.

Resource Type: software toolkit, software resource

Defining Citation: [PMID:19468054](#)

Keywords: Existing genome browsers integration, genome annotation files interface, interfacing with genome browsers

Funding: NHGRI P41 HG004059

Availability: Free, Available for download, Freely available

Resource Name: rtracklayer

Resource ID: SCR_021325

Alternate URLs: <https://github.com/lawremi/rtracklayer>

License URLs: <https://github.com/lawremi/rtracklayer/blob/master/LICENSE>

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260803T040813+0000

Ratings and Alerts

No rating or validation information has been found for rtracklayer.

No alerts have been found for rtracklayer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#).

Nitsch S, et al. (2026) H4K16 acylations destabilize chromatin architecture and facilitate transcriptional response during metabolic perturbations. *Molecular cell*, 86(1), 24.

Ahrend F, et al. (2025) Protocol for assembling, prioritizing, and characterizing piRNA clusters using the piRNA Cluster Builder. *STAR protocols*, 6(2), 103759.

Soni J, et al. (2025) Protocol for investigating intracellular microbial diversity using single-cell RNA-seq in immune cells of SARS-CoV-2-positive and recovered patients. *STAR protocols*, 6(1), 103546.

Bestehorn A, et al. (2025) Cytoplasmic mRNA decay controlling inflammatory gene expression is determined by pre-mRNA fate decision. *Molecular cell*, 85(4), 742.

Lykke-Andersen S, et al. (2024) Protocol for generating customizable and reproducible plots of sequencing coverage data using the seqNdisplayR package. *STAR protocols*, 5(2), 102960.

Chua EW, et al. (2024) A concise guide to essential R packages for analyses of DNA, RNA, and proteins. *Molecules and cells*, 47(11), 100120.

Pressl C, et al. (2024) Isolation and Molecular Profiling of Nuclei of Specific Neuronal Types from Human Cerebral Cortex and Striatum. *Current protocols*, 4(12), e70067.

Stutzman AV, et al. (2024) Heterochromatic 3D genome organization is directed by HP1a- and H3K9-dependent and independent mechanisms. *Molecular cell*, 84(11), 2017.

Lehle JD, et al. (2024) An in vitro approach reveals molecular mechanisms underlying endocrine disruptor-induced epimutagenesis. *eLife*, 13.

Fait BW, et al. (2024) Spontaneously regenerative corticospinal neurons in mice. *bioRxiv* : the preprint server for biology.

Reynolds RH, et al. (2023) Local genetic correlations exist among neurodegenerative and neuropsychiatric diseases. *NPJ Parkinson's disease*, 9(1), 70.

de Tribolet-Hardy J, et al. (2023) Genetic features and genomic targets of human KRAB-zinc finger proteins. *Genome research*, 33(8), 1409.

Mandell JD, et al. (2023) Estimation of Neutral Mutation Rates and Quantification of Somatic Variant Selection Using *cancereffectsizer*. *Cancer research*, 83(4), 500.

Mohan DR, et al. (2023) β -Catenin-Driven Differentiation Is a Tissue-Specific Epigenetic Vulnerability in Adrenal Cancer. *Cancer research*, 83(13), 2123.

van Breugel ME, et al. (2023) Locus-specific proteome decoding reveals Fpt1 as a chromatin-associated negative regulator of RNA polymerase III assembly. *Molecular cell*, 83(23), 4205.

Sturgill D, et al. (2022) Protocol for base resolution mapping of ac4C using RedaC:T-seq. *STAR protocols*, 3(4), 101858.

Dong R, et al. (2022) svaRetro and svaNUMT: modular packages for annotating retrotransposed transcripts and nuclear integration of mitochondrial DNA in genome sequencing data. *GigaByte* (Hong Kong, China), 2022, gigabyte70.

Behesti H, et al. (2021) Altered temporal sequence of transcriptional regulators in the generation of human cerebellar granule cells. *eLife*, 10.

Krchnáková Z, et al. (2019) Splicing of long non-coding RNAs primarily depends on polypyrimidine tract and 5' splice-site sequences due to weak interactions with SR proteins. *Nucleic acids research*, 47(2), 911.